

Sequence Listing

<110> Lasky, Laurence A.
Dowbenko, Donald J.

<120> Tyrosine Phosphorylated Cleavage Furrow-Associated
Proteins (PSTPIPs)

<130> P1066P2

<140> US 09/068,377

<141> 1999-05-08

<150> US 08/938,300

<151> 1997-09-29

<150> US 08/798,419

<151> 1997-02-07

<160> 73

<210> 1

<211> 415

<212> PRT

<213> Mus Musculus

<400> 1

Met	Met	Ala	Gln	Leu	Gln	Phe	Arg	Asp	Ala	Phe	Trp	Cys	Arg	Asp	1	5	10	15
Phe	Thr	Ala	His	Thr	Gly	Tyr	Glu	Val	Leu	Leu	Gln	Arg	Leu	Leu	20	25	30	
Asp	Gly	Arg	Lys	Met	Cys	Lys	Asp	Val	Glu	Glu	Leu	Leu	Arg	Gln	35	40	45	
Arg	Ala	Gln	Ala	Glu	Glu	Arg	Tyr	Gly	Lys	Glu	Leu	Val	Gln	Ile	50	55	60	
Ala	Arg	Lys	Ala	Gly	Gly	Gln	Thr	Glu	Met	Asn	Ser	Leu	Arg	Thr	65	70	75	
Ser	Phe	Asp	Ser	Leu	Lys	Gln	Gln	Thr	Glu	Asn	Val	Gly	Ser	Ala	80	85	90	
His	Ile	Gln	Leu	Ala	Leu	Ala	Leu	Arg	Glu	Glu	Leu	Arg	Ser	Leu	95	100	105	
Glu	Glu	Phe	Arg	Glu	Arg	Gln	Lys	Glu	Gln	Arg	Lys	Lys	Tyr	Glu	110	115	120	
Ala	Ile	Met	Asp	Arg	Val	Gln	Lys	Ser	Lys	Leu	Ser	Leu	Tyr	Lys	125	130	135	
Lys	Thr	Met	Glu	Ser	Lys	Lys	Ala	Tyr	Asp	Gln	Lys	Cys	Arg	Asp	140	145	150	

Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Val Ser Ala Asn Gly
155 160 165

His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys Ala Lys Gln Cys
170 175 180

Lys Glu Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg Gln Asn Ile
185 190 195

Glu Gln Leu Glu Arg Ala Arg Thr Glu Trp Glu Gln Glu His Arg
200 205 210

Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe Asp Arg Leu Thr
215 220 225

Ile Leu Arg Asn Ala Leu Trp Val His Cys Asn Gln Leu Ser Met
230 235 240

Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu Val Arg Leu Thr
245 250 255

Leu Glu Gly Cys Asp Val Glu Gly Asp Ile Asn Gly Phe Ile Gln
260 265 270

Ser Lys Ser Thr Gly Arg Glu Pro Pro Ala Pro Val Pro Tyr Gln
275 280 285

Asn Tyr Tyr Asp Arg Glu Val Thr Pro Leu Ile Gly Ser Pro Ser
290 295 300

Ile Gln Pro Ser Cys Gly Val Ile Lys Arg Phe Ser Gly Leu Leu
305 310 315

His Gly Ser Pro Lys Thr Thr Pro Ser Ala Pro Ala Ala Ser Thr
320 325 330

Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Leu Val Tyr Ala
335 340 345

Ser Ile Glu Val Gln Ala Thr Gln Gly Asn Leu Asn Ser Ser Ala
350 355 360

Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp
365 370 375

Glu Leu Asp Ile Ser Ala Gly Asp Ile Leu Ala Val Ile Leu Glu
380 385 390

Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly
395 400 405

Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu
410 415

<210> 2
<211> 2100
<212> DNA
<213> Mus Musculus

all cont
<400> 2

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attgctgata gctcattgtc cttcactttc actaacagta gcaacgggcc 150
gaacctcata acaactcaaa caaatttctca agcgctttca caaccaattg 200
cctcctctaa cgttcatgat aacttcatga ataataaat cacggctagt 250
aaaattgatg atggtataaa ttcaaaacca ctgtcacctg gttggacgga 300
ccaaactgcy tataacgcgt ttggaatcac tacagggatg tttaatacca 350
ctacaatgga tgatgtatat aactatctat tcgatgatga agatacccca 400
ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gctccttctt 450
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ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
cagaacaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
gtacaggcaa aatatgaac aactggagag agcgaggacc gagtgggagc 1300
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 tctgatgagc tggacatttc cgcgggagac atcctggcgg tcatcctgga 1850
 aggggaggat ggctggtgga ctgtggagcg gaacggacaa cgtggctttg 1900
 tccctgggtc gtacttggag aagctctgag gaaaggctag cagtctccac 1950
 atacctccgc cctgactgtg aggtcaggac tgtttcttcc catcaccgcc 2000
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 gtgctggcta ctctcaataa atgtctccca gaaggaaaaa aaaaaaaaaa 2100

<210> 3
 <211> 48
 <212> PRT
 <213> Mus Musculus

<400> 3
 Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp Glu Leu Asp Ile Ser
 1 5 10 15
 Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp
 20 25 30
 Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser
 35 40 45
 Tyr Leu Arg
 48

<210> 4
 <211> 50
 <212> PRT
 <213> Homo sapien

<400> 4
 Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn
 1 5 10 15
 Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
 20 25 30
 Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn
 35 40 45

Tyr Val Glu Lys Ile
50

<210> 5
<211> 50
<212> PRT
<213> Homo sapien

<400> 5
Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys
1 5 10 15
Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp
20 25 30
Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala
35 40 45

Tyr Val Lys Lys Leu
50

<210> 6
<211> 50
<212> PRT
<213> Homo sapien

<400> 6
Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe Asp
1 5 10 15
Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp
20 25 30
Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn
35 40 45

Tyr Val Lys Leu Leu
50

<210> 7
<211> 48
<212> PRT
<213> Homo sapien

<400> 7
Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
1 5 10 15
Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp
20 25 30
Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
35 40 45

Tyr Val Glu
48

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> 1-8
<223> Amino acid epitope tag

<400> 8
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 8

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> 1-33
<223> Synthetic oligonucleotide probe

<400> 9
cgcgatcca ccatgatggc ccagctgcag ttc 33

<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic oligonucleotide probe

<400> 10
gtacgcgtcg actcacttgt catcgctcgtc cttgtagtcg agctt 45

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic oligonucleotide probe

<400> 11
tgcctttctc tccacagg 18

<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> 1-36
 <223> Synthetic oligonucleotide probe

 <400> 12
 ctccttgagg ttctactagt gggggctggt gtcttg 36

 <210> 13
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Artificial Sequence
 <222> 1-39
 <223> Synthetic oligonucleotide probe

 <400> 13
 gcggccgcac tagtatccag tctgtgctcc atctgttac 39

 <210> 14
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Artificial Sequence
 <222> 1-17
 <223> Synthetic oligonucleotide probe

 <400> 14
 gcgtttggaa tcactac 17

 <210> 15
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic oligonucleotide probe

 <400> 15
 ttatagttta gcggccgctc accggtagtc ctgggctgat g 41

 <210> 16
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Artificial Sequence
 <222> 1-37
 <223> Synthetic oligonucleotide probe

<400> 16
 gtacgcgtcg accgcactct acgactacac tgcacag 37

<210> 17
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> 1-17
 <223> Synthetic oligonucleotide probe

<400> 17
 ctctggcgaa gaagtcc 17

<210> 18
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> 1-32
 <223> Synthetic oligonucleotide probe

<400> 18
 gatcgaattc ccagaacctc aaggagaact gc 32

<210> 19
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic oligonucleotide probe

<400> 19
 gatcctcgag ttacaccgt gtccactctg ctggagga 38

<210> 20
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic oligopeptide

<400> 20
 Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro
 1 5 10 15
 Pro Ala Glu Trp Thr
 20

<210> 21
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> 1-19
<223> Synthetic oligopeptide

<400> 21
Gly Phe Gly Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro
1 5 10 15

Pro Ser Ala Trp
19

<210> 22
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic oligopeptide

<400> 22
Gly Phe Gly Asn Arg Cys Gly Lys Pro Lys Gly Pro Arg Asp Pro
1 5 10 15

Pro Ser Glu Trp Thr
20

<210> 23
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic oligopeptide

<400> 23
Gly Gly Val Leu Arg Ser Ile Ser Val Pro Ala Pro Pro Thr Leu
1 5 10 15

Pro Met Ala Asp Thr
20

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> Artificial Sequence

<222> 1-36

<223> Synthetic oligonucleotide probe

<400> 24

gtatatgtcc tggccagccc atgggggttcc cagcag 36

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<221> Artificial Sequence

<222> 1-36

<223> Synthetic oligonucleotide probe

<400> 25

gcaggtcgac tctagattac acccgtgtcc actctg 36

<210> 26

<211> 907

<212> PRT

<213> Saccharomyces Pombe

<400> 26

Met	Leu	Thr	Lys	Ser	Leu	Gln	Gly	Ser	Glu	Asp	Ala	Gly	Met	Asp
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Ala	Leu	Met	Ser	Arg	Thr	Lys	Ser	Ser	Leu	Ser	Val	Leu	Glu	Ser
				20					25					30

Ile	Asp	Glu	Phe	Tyr	Ala	Lys	Arg	Ala	Ser	Ile	Glu	Arg	Glu	Tyr
				35					40					45

Ala	Ser	Lys	Leu	Gln	Glu	Leu	Ala	Ala	Ser	Ser	Ala	Asp	Ile	Pro
				50					55					60

Glu	Val	Gly	Ser	Thr	Leu	Asn	Asn	Ile	Leu	Ser	Met	Arg	Thr	Glu
				65					70					75

Thr	Gly	Ser	Met	Ala	Lys	Ala	His	Glu	Glu	Val	Ser	Gln	Gln	Ile
				80					85					90

Asn	Thr	Glu	Leu	Arg	Asn	Lys	Ile	Arg	Glu	Tyr	Ile	Asp	Gln	Thr
				95					100					105

Glu	Gln	Gln	Lys	Val	Val	Ala	Ala	Asn	Ala	Ile	Glu	Glu	Leu	Tyr
				110					115					120

Gln	Lys	Lys	Thr	Ala	Leu	Glu	Ile	Asp	Leu	Ser	Glu	Lys	Lys	Asp
				125					130					135

Ala	Tyr	Glu	Tyr	Ser	Cys	Asn	Lys	Leu	Asn	Ser	Tyr	Met	Arg	Gln
				140					145					150

Thr	Lys	Lys	Met	Thr	Gly	Arg	Glu	Leu	Asp	Lys	Tyr	Asn	Leu	Lys
				155					160					165

Ile Arg Gln Ala	Ala Leu Ala Val Lys	Lys Met Asp Ala Glu Tyr	170	175	180
Arg Glu Thr Asn	Glu Leu Leu Leu Thr	Val Thr Arg Glu Trp Ile	185	190	195
Asp Arg Trp Thr	Glu Val Cys Asp Ala	Phe Gln His Ile Glu Glu	200	205	210
Tyr Arg Leu Glu	Phe Leu Lys Thr Asn	Met Trp Ala Tyr Ala Asn	215	220	225
Ile Ile Ser Thr	Ala Cys Val Lys Asp	Asp Glu Ser Cys Glu Lys	230	235	240
Ile Arg Leu Thr	Leu Glu Asn Thr Asn	Ile Asp Glu Asp Ile Thr	245	250	255
Gln Met Ile Gln	Asn Glu Gly Thr Gly	Thr Thr Ile Pro Pro Leu	260	265	270
Pro Glu Phe Asn	Asp Tyr Phe Lys Glu	Asn Gly Leu Asn Tyr Asp	275	280	285
Ile Asp Gln Leu	Ile Ser Lys Ala Pro	Ser Tyr Pro Tyr Ser Ser	290	295	300
Ser Arg Pro Ser	Ala Ser Ala Ser Leu	Ala Ser Ser Pro Thr Arg	305	310	315
Ser Ala Phe Arg	Pro Lys Thr Ser Glu	Thr Val Ser Ser Glu Val	320	325	330
Val Ser Ser Pro	Pro Thr Ser Pro Leu	His Ser Pro Val Lys Pro	335	340	345
Val Ser Asn Glu	Gln Val Glu Gln Val	Thr Glu Val Glu Leu Ser	350	355	360
Ile Pro Val Pro	Ser Ile Gln Glu Ala	Glu Ser Gln Lys Pro Val	365	370	375
Leu Thr Gly Ser	Ser Met Arg Arg Pro	Ser Val Thr Ser Pro Thr	380	385	390
Phe Glu Val Ala	Ala Arg Pro Leu Thr	Ser Met Asp Val Arg Ser	395	400	405
Ser His Asn Ala	Glu Thr Glu Val Gln	Ala Ile Pro Ala Ala Thr	410	415	420
Asp Ile Ser Pro	Glu Val Lys Glu Gly	Lys Asn Ser Glu Asn Ala	425	430	435
Ile Thr Lys Asp	Asn Asp Asp Ile Ile	Leu Ser Ser Gln Leu Gln	440	445	450

Pro Thr Ala Thr Gly Ser Arg Ser Ser Arg Leu Ser Phe Ser Arg	455	460	465
His Gly His Gly Ser Gln Thr Ser Leu Gly Ser Ile Lys Arg Lys	470	475	480
Ser Ile Met Glu Arg Met Gly Arg Pro Thr Ser Pro Phe Met Gly	485	490	495
Ser Ser Phe Ser Asn Met Gly Ser Arg Ser Thr Ser Pro Thr Lys	500	505	510
Glu Gly Phe Ala Ser Asn Gln His Ala Thr Gly Ala Ser Val Gln	515	520	525
Ser Asp Glu Leu Glu Asp Ile Asp Pro Arg Ala Asn Val Val Leu	530	535	540
Asn Val Gly Pro Asn Met Leu Ser Val Gly Glu Ala Pro Val Glu	545	550	555
Ser Thr Ser Lys Glu Glu Asp Lys Asp Val Pro Asp Pro Ile Ala	560	565	570
Asn Ala Met Ala Glu Leu Ser Ser Ser Met Arg Arg Arg Gln Ser	575	580	585
Thr Ser Val Asp Asp Glu Ala Pro Val Ser Leu Ser Lys Thr Ser	590	595	600
Ser Ser Thr Arg Leu Asn Gly Leu Gly Tyr His Ser Arg Asn Thr	605	610	615
Ser Ile Ala Ser Asp Ile Asp Gly Val Pro Lys Lys Ser Thr Leu	620	625	630
Gly Ala Pro Pro Ala Ala His Thr Ser Ala Gln Met Gln Arg Met	635	640	645
Ser Asn Ser Phe Ala Ser Gln Thr Lys Gln Val Phe Gly Glu Gln	650	655	660
Arg Thr Glu Asn Ser Ala Arg Glu Ser Leu Arg His Ser Arg Ser	665	670	675
Asn Met Ser Arg Ser Pro Ser Pro Met Leu Ser Arg Arg Ser Ser	680	685	690
Thr Leu Arg Pro Ser Phe Glu Arg Ser Ala Ser Ser Leu Ser Val	695	700	705
Arg Gln Ser Asp Val Val Ser Pro Ala Pro Ser Thr Arg Ala Arg	710	715	720
Gly Gln Ser Val Ser Gly Gln Gln Arg Pro Ser Ser Ser Met Ser	725	730	735

Leu	Tyr	Gly	Glu	Tyr	Asn	Lys	Ser	Gln	Pro	Gln	Leu	Ser	Met	Gln	
				740					745					750	
Arg	Ser	Val	Ser	Pro	Asn	Pro	Leu	Gly	Pro	Asn	Arg	Arg	Ser	Ser	
				755					760					765	
Ser	Val	Leu	Gln	Ser	Gln	Lys	Ser	Thr	Ser	Ser	Asn	Thr	Ser	Asn	
				770					775					780	
Arg	Asn	Asn	Gly	Gly	Tyr	Ser	Gly	Ser	Arg	Pro	Ser	Ser	Glu	Met	
				785					790					795	
Gly	His	Arg	Tyr	Gly	Ser	Met	Ser	Gly	Arg	Ser	Met	Arg	Gln	Val	
				800					805					810	
Ser	Gln	Arg	Ser	Thr	Ser	Arg	Ala	Arg	Ser	Pro	Glu	Pro	Thr	Asn	
				815					820					825	
Arg	Asn	Ser	Val	Gln	Ser	Lys	Asn	Val	Asp	Pro	Arg	Ala	Thr	Phe	
				830					835					840	
Thr	Ala	Glu	Gly	Glu	Pro	Ile	Leu	Gly	Tyr	Val	Ile	Ala	Leu	Tyr	
				845					850					855	
Asp	Tyr	Gln	Ala	Gln	Ile	Pro	Glu	Glu	Ile	Ser	Phe	Gln	Lys	Gly	
				860					865					870	
Asp	Thr	Leu	Met	Val	Leu	Arg	Thr	Gln	Glu	Asp	Gly	Trp	Trp	Asp	
				875					880					885	
Gly	Glu	Ile	Ile	Asn	Val	Pro	Asn	Ser	Lys	Arg	Gly	Leu	Phe	Pro	
				890					895					900	
Ser	Asn	Phe	Val	Gln	Thr	Val									
				905		907									

<210> 27

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<221> Any amino acid

<222> 2-3

<223> Any amino acid

<400> 27

Pro Xaa Xaa Pro

1 4

<210> 28

<211> 1613

<212> DNA

<213> Homo sapien

<400> 28

acgatcacta tagggcgaat tgggcctcta gatgcatgct cgagcggccg 50

ccagtgtgat ggatatctgc agaattcggc ttccatccta atacgactca 100
 ctatagggct cgagcggccg cccgggcagg tctagaattc agcggccgct 150
 gaattctctt tttcctcccc tcagaagctc ctctctggct cgtggctgcc 200
 ttctgagtgt tgcagacggc gccggccggg aagggggggc tgggccagcc 250
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 gcggacgacg cggagcaggc cttcgagcgc attagcgcca acggccacca 900
 gaagcagggtg gagaagagtc agaacaaagc caggcagtgc aaggactcgg 950
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 gagaccctga cccccacccc cgagcggaat gaggggtgtct acacagccat 1350
 cgcagtgcag gagatacagg gaaaccggc ctcaccagcc caggactacc 1400
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cgggcagcgt ggcttcgtcc ctggttccta cctggagaag ctttgagggga 1550
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 ccccagcact gtc 1613

<210> 29
 <211> 400
 <212> PRT
 <213> Homo sapien

<400> 29
 Met Met Pro Gln Leu Gln Phe Lys Asp Ala Phe Trp Cys Arg Asp
 1 5 10 15
 Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu
 20 25 30
 Asp Gly Arg Lys Met Cys Lys Asp Met Glu Glu Leu Leu Arg Gln
 35 40 45
 Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile
 50 55 60
 Ala Arg Lys Ala Gly Gly Gln Thr Glu Ile Asn Ser Leu Arg Ala
 65 70 75
 Ser Phe Asp Ser Leu Lys Gln Gln Met Glu Asn Val Gly Ser Ser
 80 85 90
 His Ile Gln Leu Ala Leu Thr Leu Arg Glu Glu Leu Arg Ser Leu
 95 100 105
 Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Gly Met
 110 115 120
 Ala Val Pro Arg Gln Ser Asp Cys Met Glu Val Lys Ser Pro Ser
 125 130 135
 Trp Glu Tyr Glu Ala Val Met Asp Arg Val Gln Lys Ser Lys Leu
 140 145 150
 Ser Leu Tyr Lys Lys Ala Met Glu Ser Lys Lys Thr Tyr Glu Gln
 155 160 165
 Lys Cys Arg Asp Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Ile
 170 175 180
 Ser Ala Asn Gly His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys
 185 190 195
 Ala Arg Gln Cys Lys Asp Ser Ala Thr Glu Ala Glu Arg Val Tyr
 200 205 210
 Arg Gln Ser Ile Ala Gln Leu Glu Lys Val Arg Ala Glu Trp Glu
 215 220 225

Gln	Glu	His	Arg	Thr	Thr	Cys	Glu	Ala	Phe	Gln	Leu	Gln	Glu	Phe	230	235	240
Asp	Arg	Leu	Thr	Ile	Leu	Arg	Asn	Ala	Leu	Trp	Val	His	Ser	Asn	245	250	255
Gln	Leu	Ser	Met	Gln	Cys	Val	Lys	Asp	Asp	Glu	Leu	Tyr	Glu	Glu	260	265	270
Val	Arg	Leu	Thr	Leu	Glu	Gly	Cys	Ser	Ile	Asp	Ala	Asp	Ile	Asp	275	280	285
Ser	Phe	Ile	Gln	Ala	Lys	Ser	Thr	Gly	Thr	Glu	Pro	Pro	Arg	Phe	290	295	300
Ser	Gly	Leu	Leu	His	Gly	Ser	Pro	Lys	Thr	Thr	Ser	Ser	Ala	Ser	305	310	315
Ala	Gly	Ser	Thr	Glu	Thr	Leu	Thr	Pro	Thr	Pro	Glu	Arg	Asn	Glu	320	325	330
Gly	Val	Tyr	Thr	Ala	Ile	Ala	Val	Gln	Glu	Ile	Gln	Gly	Asn	Pro	335	340	345
Ala	Ser	Pro	Ala	Gln	Asp	Tyr	Arg	Ala	Leu	Tyr	Asp	Tyr	Thr	Ala	350	355	360
Gln	Asn	Pro	Asp	Glu	Leu	Asp	Leu	Ser	Ala	Gly	Asp	Ile	Leu	Glu	365	370	375
Gly	Glu	Asp	Gly	Trp	Trp	Thr	Val	Glu	Arg	Asn	Gly	Gln	Arg	Gly	380	385	390
Phe	Val	Pro	Gly	Ser	Tyr	Leu	Glu	Lys	Leu						395	400	

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<220>

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<210> 31

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 <211> 45
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 <400> 55
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 ggatggtgag ccggtctgcc tcctgcagct ggaggcc 37
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<400> 58
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<400> 59
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<400> 60
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<210> 64

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<211> 36

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<210> 67

<211> 33

<212> DNA

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<400> 69
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<400> 70
ggaggatctc gggccccttt ggccttcg 30

<210> 71
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<400> 71
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<223> Synthetic oligonucleotide probe

<400> 72

gtccactctg cagcaggatc ccggggccct t 31

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<211> 34

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<400> 73

gttacaccg tgtcgcctct gcaggaggat cccg 34